Chicken a Chicken a Vp3 (apop HIV TAT t Maltose b

Aam51138 Aam51139 Human apo Human apo

Ade52808 Ade52808 Ade52806 Ade52806 Ade52806 Ade52806 Ade13010 Adula010 Adula010 Adul98745

Human apo Apoptin 1 Chicken a Chicken a Chicken a

Human apo Human apo Human apo Human apo

Aau98746 Aau98746 Aau98749 Ade52798 Ade52821 Ade52818

Chicken a Human apo Human apo

Aau98747 (Ade52800 F

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Immunogenic peptide, apoptin; cancer; leukaemia; p53; apoptosis; mutein; cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bcl-2; gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant; Bcl-2-associating protein; BAG-1; cell proliferation disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells or cancer prone cells, and for treating cancer or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated or recombinant phosphorylated Apoptin (I) also known as VP3 or its functional equivalent and/or its functional fragment. Apoptin induces apoptosis in human malignant and transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild-type Lys substituted by Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken anemia virus synthesised apoptin protein.
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            AAU98759
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                                                                                                                                                                                                                                                                                                                                                             AAU98742 standard; peptide; 121
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20-OCT-2000; 2000US-0242397P
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Chicken anemia virus
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Misc-difference
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            Synthetic
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1 MNALQEDTPPGPSTVFRPPT.......ESLITTTPSRPRTARRIRL 121
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                                                                                          December 23, 2004, 10:36:00 ; Search time 155 Seconds
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Compugen Ltd.
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                                                                                                                                                                                                                                       2002273 seqs, 358729299 residues
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Copyright (c) 1993 - 2004
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Listing first 45 summaries
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cc selective destruction of tumour cells which are resistant to chemotherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be phosphorylated and a nucleic acid encoding a kinase capable of phosphorylated and a nucleic acid encoding a kinase capable of comprising apoptin, a gene delivery vehicle comprising the vector, a concleic acid encoding the antibody, a vector comprising the antibody a nucleic acid a host cell comprising the antibody nucleic acid a host cell comprising the antibody mucleic acid a host cell comprising the antibody nucleic acid a host cell comprising the antibody nucleic acid or vector. Apoptin is useful for diagnostic purposes, for detecting the presence of cancer inducing agent, for testing the in vitro treatment effect of apoptin on tumour cells and for identifying a tumour specific kinase. Compositions comprising the apoptins and attmoor specific kinase. Compositions comprising the apoptins and attmoor specific compound for treating an individual carrying a disease where enhanced cell correcting an individual carrying a disease where enhanced cell correcting an individual carrying a disease where enhanced cell correcting an individual carrying a theory correction of tumour cells or hyperplasia, metaplasia or dysplasia, Apoptin has no toxic effect in in vivo treatment regimes and induces apopton has no toxic effect in in vivo treatment regimes and induces apopton the Bcl-2 associating protein BAG-1. The present sequence is a synthesised apoptin containing a Lys to Arg mutation at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 632; DB 5;
; Pred. No. 2.5e-61;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LEAD-) LEADD BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  position 116
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New fragment of Apoptin that induces aberrant-specific apoptosis, useful in preparing a medicament for treating a disease associated with enhanced cell proliferation or decreased cell death, e.g., cancer or autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "These 5 residues are replaced by Ala-Ala-Ala-Ala-Ala Ala in a loss-of-function mutant created in the
                                                                                                                          The invention relates to a novel isolated or recombinant fragment of Apoptin that is capable of inducing aberrant-specific apoptosis. A peptide of the invention has cytostatic, and immunosuppressive activity, and may have a use in gene therapy. The fragment of Apoptin, nucleic acid, vector, gene delivery vehicle or host cell is useful in preparing additionant for treating a disease where enhanced cell proliferation or decreased cell death is observed, e.g., cancer or autoimmune disease. The present sequence is used in the exemplification of the invention.
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/note= "These 2 residues are replaced by Ala-Ala in a
loss-of-function mutant created in the invention"
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specific Apoptin kinase (tumour-specific kinase)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptin; VP3; CAV; tumour-specific phosphorylation; tumour-specific kinase; endogenous substrate; identification; kinase inhibitor; kinase modulator; cell proliferative disorder; apoptotic disorder; autoimmune disease; cycostatic;
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                                                                                                                                                                                                                                                                                                                              Length 121;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                            100.0%; Score 632; DB 7;
100.0%; Pred. No. 2.5e-61;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken anaemia virus (CAV) Apoptin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM13007 standard; protein; 121 AA.
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                                                                                          2; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-2003; 2003WO-NL000294.
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 121, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 106. .110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken anemia virus.
                                                                                                                                                                                                                                                                                            Sequence 121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM13007;
                                                        disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                          Claim
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ADM13007
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(revised) (first entry)

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Chicken anemia virus VP1 protein; apoptosis; cancer therapy; vaccine;
                                                                                                                                        antitumor; antibody generation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 3; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for inducing apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                         Noteborn MHM, Koch G;
                                                                                                                                                                           Chicken anemia virus.
                                                                                                                                                                                                                                                                                                                                                      (AESC-) AESCULAAP BV
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-075240/10.
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                                                                                                                                                                                                              WO9503414-A2
                                                                                                                                                                                                                                                                                   19-JUL-1994;
                                                                                                                                                                                                                                                                                                                    20-JUL-1993;
                                  25-MAR-2003
19-AUG-1995
                                                                                                                                                                                                                                                02-FEB-1995
                                                                                       7P3 protein
AAR65201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicken
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                                                                                                                                                                                                                                                                        The invention relates to a method for identifying a substrate of a kinase capable of phosphorylating Apoptin (also known as VP3) in a manner.
Characteristic of malignant and transformed cells (abbrant cells).
Characteristic of malignant and transformed cells (abbrant cells).
Choptin is a small protein derived from chicken anaemia virus (CAV) which induces apoptosis in malignant and transformed cells, but not in normal cells. The pattern of apoptotic activity is related to the finding that composin is phosphorylated on Thr 108 in aberrant cells, whereas it is not phosphorylated at this position in normal cells, indicating that there is a tumour-specific kinase activity. The method of the invention aims to identify endogenous cellular substrates for this tumour-specific kinase civity. The method of the invention aims to identify endogenous cellular substrates for this mourabenge the components of the lysates with a molecule capable of recognising phosphorylated Apoptin and phosphorylated aubstrate; and visualising the molecule, comparing the lysate components and identifying the above method; a method of obtaining a modulator of a kinase involved in aberrant-specific Apoptin phosphorylation; a protein inhibitor of an inhibitor; vectors, host cells and gene delivery vehicles comprised in aberrant cells and gene delivery vehicles comprised in aberrant cells and gene delivery vehicles comprised to the mothod of the binds to both aberrant cells and gene delivery vehicles comprised of the cording to the method of the cinvention is useful as a drug target. The inhibitor, nucleic acid cording to the method of a tumour-specific kinase substrate identified according to the method of the invention is useful as a drug target. The inhibitor is useful in the treatment of disease where enhanced cell problement of disease where enhanced cell problement is observed, e.g., cancer or autoimmune diseases.

The tumour-specific kinase substrate identified according to the method of the invention is useful as a drug target for these m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                     Identifying a substrate of a kinase capable of phosphorylating Apoptin in an aberrant-specific way, useful in inducing apoptosis in tumor cells, comprises preparing aberrant and reference cells and incubating with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TADNSESTGFKONVPDLATDOPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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100.0%; Pred. No. 2.5e-61;
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                                                                                                                                                                                                                                                Example; Fig 1; 69pp; English
                  19-APR-2002; 2002EP-00076596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 121; Conservative
                                                                                     Noteborn MHM, Rohn JL;
                                                                                                                        WPI; 2003-845561/78.
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                                                   (LEAD-) LEADD BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptin kinase.
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Best:Local &
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anaemia virus (CAV) mutant polypeptide(s) - useful as vaccines

94WO-NL000168. 93NL-00001272.

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                                                                                                                                                                                                                                                                             61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRRIR 120
                                                                                                                                                                                                                                                                                              61 TADNSESTGFKNVPDLATDQPKPPSKKRSCDPSEYRVSELKBSLITTTPSRPRTAKRRR 120
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                                                                                                                                                                                                      1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                         MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                    Gaps
The sequence corresponds to a VP3 protein from chicken anemia virus, (CAV), and may be used to induce apoptosis directly or to generate antibodies against CAV. The protein may be used as a vaccine or an antitumor agent. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken infectious anaemia virus; vaccination; VP1; VP2; VP3; ss.
                                                                                                                              Length 121;
                                                                                                                                                                0; Indels
                                                                                                                            Score 629; DB 2;
Pred. No. 5.3e-61;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicken anemia virus (usa isolate CIA-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VP3 of chicken infectious anaemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR88499 standard; protein; 121 AA.
                                                                                                                                99.58;
                                                                                                                                                   99.28;
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                                                                                                                                                                    Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                 Local Similarity
                                                                                           Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                       121 L 121
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15-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                Query Match
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AAR65201 standard; protein; 121 AA.

RESULT 4 AAR65201

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The present invention describes a fusion molecule (I) comprising at least one protein transduction domain (PTD) and at least one chicken anaemia virus (CAV) VP3 molecule. (I) has cytostatic activity and can be used for inducing cell death. (I) is useful for detecting cancerous or precancerous cells in a mammal. (I) is useful as a magnetic bullet to cancerous cells in a mammal. (I) is useful as a magnetic bullet to selectively kill cancer cells in vitro and in vivo, for inducing cell death, and for preventing or treating cancer and related proliferative disorders. (I) is also useful for studying mechanisms of carcinogenesis and materiasses eukaryotic cells. (I) effectively transduces VP3 molecules directly into the cells. (I) attacks cancer and pre-cancerous cells while leaving normal cells relatively unharmed. Since more cells can be targeted by (I) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents the CAV VP3 protein sequence which is given in the exemplification of the present invention
                                                                                                                                Novel fusion molecule useful for preventing or treating cancer, comprises a protein transduction domain and a chicken anemia virus VP3 molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TADNSESTGFKAVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic peptide, apoptin; cancer; leukaemia; p53; apoptosis; mutein; cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bc1-2; gene therapy; hyperplasia; metaplasia; dysplasia; Bc1-2; Bc1-2; Bc1-2-associating protein; BAG-1; cell proliferation disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.5%; Score 629; DB 6; Length 121; 99.2%; Pred. No. 5.3e-61;
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                                                                                                                                                                                                       Disclosure; Page 22; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
Misc-difference 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU98752 standard; peptide; 121 AA.
                                             Wadia JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alanine scanning; phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 120; Conservative
                                             Ezhevsky SA,
(UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicken anemia virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 121 AA;
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                                             Dowdy SF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
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                                                                                                                                                                                                                                                                                                                                                                                                                                               The genome of the CIA-1 strain of chicken infectious anaemia virus encodes a VP-1 protein with at least four unique amino acid changes compared to the VP1 protein of other chicken infectious anaemia virus isolates. The new VP1 amino acid sequence exhibits a difference in pathogenic potential and cell tropism as compared to cell culture-adapted strains. New sequences (encoding VP1 (AAT10911), VP2 (AAT10912) and VP3 (AAT10913)) and the corresponding polypeptides may be used in strategies to control chicken infectious anaemia such as by vaccination. (Updated on
                                                                                                                                                                                                                                                                                                               Chicken infectious anaemia virus strain CIA-1 genome sequences, and novel VP1, sequence - useful to control chicken infectious anaemia such as by vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121;
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Pred. No. 5.3e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                    Lucio B, Renshaw R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken anaemia virus (CAV) VP3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 43-44; 59pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2003 to correct OS field.)
                                                                                                                                                     (CORR ) CORNELL RES FOUND INC
                                          95WO-US008440.
                                                                                     95US-00271094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%;
99.2%;
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                                                                                                                                                                                             Schat KA, Soine C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chicken anemia virus
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Best Local Similarity
                                                                                                                                                                                                                                                                    N-PSDB; AAT10913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 121 AA;
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                                     05-JUL-1995;
                                                                                                          03-JUL-1995;
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유 ò ద ò 유 9

Gaps

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cytostatic, autoimmune disease, immunosuppressive, VP3, tumour, Bc1-2, gene therapy, hyperplasia, metaplasia, dysplasia, Bcr-abl; mutant, Bc1-2-associating protein, BAG-1, cell proliferation disorder,

alanine scanning; phosphorylation.

Chicken anemia virus.

Synthetic.

/note= "Wild-type Thr substituted by Ala"

. Misc-difference 106

WO200232954-A2

25-APR-2002

19-OCT-2001; 2001WO-NL000771. 20-OCT-2000; 2000EP-00203652. 20-OCT-2000; 2000US-0242397P.

apoptin; cancer; leukaemia; p53; apoptosis;

Chicken anemia virus apoptin T106A mutant.

Immunogenic peptide;

(first entry)

27-AUG-2002

AAU98750;

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The invention relates to an isolated or recombinant phosphorylated
Apoptin (I) also known as VP3 or its functional equivalent and/or its
Cunctional fragment. Apoptin induces apoptosis in human malignant and
transformed cell lines but not in untransformed cells, by a p52
Cundependent mechanism. Apoptin is therefore a candidate therapeutic for
independent mechanism. Apoptin is therefore a candidate therapeutic for
selective destruction of tumour cells which are resistant to
chemotherapeutic agents inducing p53/P61-2 associated apoptosis. Also
concluded are a vector comprising a nucleic acid encoding apoptin, (or its
functional equivalent and/or its functional fragment) which can be
concerned and a nucleic acid encoding a kinase capable of
concleic acid encoding the antibody, a vector comprising the vector, a
concer cells cacid encoding the antibody in antibody a
concer cells a host cell comprising the antibody incleic acid acid encoding the antibody incleic acid or vector,
concerning agent, for testing the antibody nucleic acid or vector,
concerninducing agent, for testing the in vitro treatment effect of
cancer cells or cells that are cancer prone, for identifying a putative
cancer-inducing agent, for testing the in vitro treatment effect of
cancer-inducing agent, for testing the in vitro treatment effect of
cancer-inducing agent, for testing the in vitro treatment effect of
conpositions comprising the apoptins and antibodies are useful for
treating an individual carrying a disease where enhanced cell
confortieration or decreased cell death is observed, e.g. cancer,
confortieration or decreased cell death is observed, e.g. cancer,
confortieration or decreased cell death is observed, e.g. cancer,
confortieration or decreased cell death is observed, e.g. cancer,
confortieration or decreased cell death is observed, e.g. cancer,
confortieration or decreased cell death is observed, e.g. cancer,
confortieration or decreased cell death is observed, e.g. cancer,
confortieration or decreased cell death is observed, e.g. 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells or cancer prone cells, and for treating cancer or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                    Donner P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page; 62pp; English.
19-OCT-2001; 2001WO-NL000771.
                                                                                                     20-OCT-2000; 2000EP-00203652.
20-OCT-2000; 2000US-0242397P.
                                                                                                                                                                                                                                                                                                                                                                                                    Rohn JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-463306/49.
                                                                                                                                                                                                                                                                                   (LEAD-) LEADD BV.
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Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells or cancer prone cells, and for treating cancer or autoimmune disease.

Disclosure, Page, 62pp, English.

Donner P;

Mumberg D,

Noteborn MHM, Rohn JL,

(LEAD-) LEADD BV.

WPI; 2002-463306/49.

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Apoptin (I) also known as VP3 or its functional equivalent and/or its Apoptin (I) also known as VP3 or its functional equivalent and/or its functional fragment. Apoptin induces apoptosis in human malignant and transformed cell lines but not in untransformed cells, by a p53 cross-configuration of tumour cells which are resistant to chemotherapeutic agents inducing p53/BC1-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be phosphorylating apoptin, a gene delivery vehicle comprising the vector. Comprising the vector or vehicle, an anti-apoptin antibody, a nucleic acid encoding the antibody a vector comprising the presence of concer cells and encoding the antibody nucleic acid or vector. Apoptin is useful for diagnostic purposes, for detecting the presence of cancer cells or cells that are cancer prone, for identifying a putative cancer cells or cells that are cancer prone, for identifying a putative cancer-inducing agent, for testing the in vitro treatment effect of apoptin on tumour cells, and for identifying a tumour specific kinase. Compositions comprising the apoptin a disease where enhanced cell care treating an individual carrying a disease where enhanced cell cor auto-immune disease. Apoptin is useful as a therapeutic compound for the selective destruction of tumour cells or hyperplasia, metaplasia or dysplasia. Apoptin has no toxic effect in in vivo treatment regimes and induces apoptosis in the absence of functional p53 and cannot be blocked by printing and antibodies. The present cancer in the present and proving a parating and proving a parating present and proving and antibodies. The present and proving and antibodies and cannot be blocked and proving and antibodies apoptines and proving and antibodies and cannot be plocked and antibodies.
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Pred. No. 1.9e-60;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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protein sequence Sequence 121 AA

AAU98750 standard; peptide; 121 AA.

AAU98750 ID AAU9 XX RESULT 8

121 L 121 Ĺ 121

121

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Query Match

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concleic acid encoding the antibody, a vector comprising the antibody, a nucleic acid encoding the antibody, a vector comprising the antibody nucleic acid or vector, anucleic acid, a host cell comprising the antibody nucleic acid or vector, Apoptin is useful for diagnostic purposes, for detecting the presence of cancer rinducing agent, for testing the in vitro treatment effect of apoptin on tumour cells, and for identifying a tumour specific kinase. Compositions comprising the apoptins and antibodies are useful for treating an individual carrying a disease where enhanced cell compositions or decreased cell death is observed, e.g. cancer, leukaemia or treating an individual carrying a disease where enhanced cell to a vector auto-immune disease. Apoptin is useful as a therapeutic compound for the selective destruction of tumour cells or hyperplasia metaplasia or dysplasia. Apoptin has no toxic effect in in vivo treatment regimes and induces apoptin mutant created functional. P53 and cannot be blocked by Bcl-2, Bcr-abl or the Bcl-2-associating protein BAG-1. The present esquence is an apoptin mutant created during an alanine scanning experiment for mapping the phosphorylation sites in apoptin in figure 4 and the wild-type apoptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel fusion molecule useful for preventing or treating cancer, comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TADNSESTGFKAVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNALQEDTPPGESTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 624; DB 5; Length 121; Pred. No. 1.9e-60; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP56092 standard; protein; 190 AA.
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Matches 119; Conservative
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N-PSDB; ABZ21714.
                                                                                                                                                                                                                                                                                                                                                                 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121 AA;
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ABP56092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated or recombinant phosphorylated Apoptin (1) also known as VP3 or its functional equivalent and/or its functional regament. Apoptin induces apoptosis in human malignant and transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic for selective destruction of tumour cells which are resistant to chemocherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be phosphorylated and a nucleic acid encoding a kinase capable of phosphorylating apoptin, a gene delivery vehicle comprising the vector, a
                                                                                                                                                                                                 TADNSESTGFKNVPDLRTDOPKPPSKKRSCDPSEYRVSELKESLIATTPSRPRTAKRIR 120
                                                                                                                                                                            TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; autoimmune disease; lemkaemia; p53; apoptosis; mutein; cytostatic; autoimmune disease; immunosuppressive; VF3; tumour; Bcl-2; gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-ab1; mutant; Bcl-2-associating protein; BAG-1; cell proliferation disorder; alanine scanning; phosphorylation.
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                                                                                                                        1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITILLSLCGCANARAPTLRSA
                                                                                                     1 MNALQEDIPPGPSTVFRPPISSRPLEIPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                 Gaps
                                                                 ;
0
                          Length 121;
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                                                                 1; Indels
                            Score 624; DB 5;
Pred. No. 1.9e-60;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken anemia virus apoptin T107A mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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20-OCT-2000; 2000US-0242397P
                            98.7%;
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                                                                 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-463306/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 107
                                               Similarity
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                            Query Match
Best Local S
Matches 119
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAU98751;
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Gaps

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us-10-083-849b-1.rag

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The present invention describes a fusion molecule (I) comprising at least one protein transduction domain (PTD) and at least one chicken anaemia virus (CAN) VP3 molecule. (I) has cytostatic activity and can be used for inducing cell death. (I) is useful for detecting cancerous or precancerous cells in a mammal. (I) is useful as a magnetic bullet to cancerous cells in a mammal. (I) is useful as a magnetic bullet to cancerous cells in a mammal. (I) is useful as a magnetic bullet to death, and for preventing or treating cancer and related proliferative clastrates. (I) is also useful for studying mechanisms of carcinogenesis and metastases eukaryotic cells. (I) effectively transduces VP3 molecules discotly into the cells. (I) afteates ancer and pre-cancerous cells while targetly into the cells. (I) afteates ancer and pre-cancerous cells while leaving normal cells relatively unharmed. Since more cells can be targeted by (I) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents a TAT-VP3 fusion protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 NALQEDTPPGESTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSAT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a fusion molecule (I) comprising at least
a protein transduction domain and a chicken anemia virus VP3 molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 624; DB 6;
Pred. No. 3.3e-60;
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                                     Claim 36; Fig 2; 104pp; English.
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                                                                                                                                                                                                                                                                                                                                                               the present invention
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 190 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119;
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            virus (CAV) VP3 molecule. (I) has cytostatic activity and can be used for inducing cell death. (I) is useful for detecting cancerous or precancerous cells in a mammal. (I) is useful as a magnetic bullet to cancerous cells in a mammal. (I) is useful as a magnetic bullet to selectively kill cancer cells in vitro and in vivo, for inducing cell death, and for preventing or treating cancer and related proliferative disorders. (I) is also useful for studying mechanisms of carcinogenesis and metastases cukaryotic cells. (I) effectively transduces VP3 molecules directly into the cells. (I) attacks cancer and pre-cancerous cells while leaving normal cells relatively unharmed. Since more cells can be targeted by (I) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents a PTD4-VP3 fusion protein from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIRL 121
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                                                                                                                                                                                                                                                                                                                                                         Score 624; DB 6; Length 190;
Pred. No. 3.3e-60;
1; Mismatches 0; Indels
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nes 119; Conservative
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                                                                                                                                                                                                                                                                                                                        Sequence 190 AA;
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death, and for preventing or treating cancer and related proliferative disorders. (I) is also useful for studying mechanisms of carcinogenesis and metastases eukaryotic cells. (I) effectively transduces VP3 molecules directly into the cells. (I) affectively transduces VP3 molecules directly into the cells. (I) attacks cancer and pre-cancerous cells while leaving normal cells relatively unharmed. Since more cells can be targeted by (I) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents a PTD5-VP3 fusion protein from the present invention
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Pred. No. 3.3e-60;
1; Mismatches 0;
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99.2%;
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Matches 119, Conservative
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                                                                                                                                                                                                                  Sequence 190 AA;
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The present invention describes a fusion molecule (I) comprising at least one protein transduction domain (PTD) and at least one chicken anaemia cone protein transduction domain (PTD) and at least one chicken anaemia control of the concerous (C) is useful for detecting cancerous or precancerous cells in a mammal. (I) is useful as a magnetic bullet to cancerous cells in a mammal or for killing or injuring cancerous or precancerous cells in a mammal or for killing or injuring cancerous or precancerous cells in a mammal or for killing or injuring cancerous or precancerous cells in a mammal or for killing or injuring cancerous or precancerous cells in a mammal or for killing and in vivo, for inducing cell death, and for preventing or treating cancer and related proliferative cliscofars. (I) is also useful for studying mechanisms of carcinogeneesis and metastases eukaryotic cells. (I) effectively transduces VP3 molecules cliscotly into the cells. (I) attacks cancer and pre-cancerous cells while leaving normal cells relatively unharmed. Since more cells can be cargeded by (I) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present septembers a TAT-GST-VP3 fusion protein
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leaving normal cells relatively unharmed. Since more cells can be targeted by (1) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents a PTD3-VP3 fusion protein from
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                                                                                                                                                            Score 624; DB 6; Length 190;
Pred. No. 3.3e-60;
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Best Local Similarity
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                                                                                                                        Sequence 190 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 ADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRIRL 422
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                                                                                                                                            Length 422;
                                                                                                                                                                                                               0; Indels
                                                                                                                                         Score 624; DB 6;
Pred. No. 8.6e-60;
1; Mismatches 0
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Best Local Similarity 99.2%;
Matches 119; Conservative
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from the present invention
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                                                                      Sequence 422 AA;
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from the present invention

Sequence 432 AA;

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                                                                             2 NALOEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSAT
                                         Gaps
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98.7%; Score 624; DB 6; Length 432; 99.2%; Pred. No. 8.8e-60; ive 1; Mismatches 0; Indels
 Query Match
Best Local Similarity 99.2
Matches 119; Conservative
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Search completed: December 23, 2004, 11:00:10 Job time : 157 secs

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COMPUTER FALCABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPUTER:
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: US/08/489,666C
FILING DATE: US/08/489,666C
FILING DATE: US/08/489,666C
FILING DATE: US/08/489,666C
FILING DATE: US 08/454,121
PRIOR APPLICATION NUMBER: US 08/454,121
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL 94/00168
FILING DATE: 19-JUL-1994
PRIOR APPLICATION NUMBER: PCT/NL 91/00165
FILING DATE: 10-5-UL-1991
FRIOR APPLICATION NUMBER: NL 9301272
FILING DATE: 10-101-1993
FILING DATE: 12-SPE-1991
FRIOR APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SPE-1990
APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SPE-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAB-VENTER, BARBARA
REGISTRATION NUMBER: LEBV.003.04US
TELEPHONE: (650)328-4400
                                                                                                                                                                                                                                                                                                                                                     US-08-489-666C-7
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STATE:
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 25, Appli
Sequence 25313, A
Sequence 24227, A
Sequence 2438, A
Sequence 41118, A
Sequence 41118, A
Sequence 41118, A
Sequence 41387, A
Sequence 41387, A
Sequence 2938, A
Sequence 2938, A
Sequence 20318, A
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                                                                                                               (without alignments)
211.170 Million cell updates/sec
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1 MNALOEDTPPGPSTVFRPPT......ESLITTTPSRPRTARRIRL 121
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                                                                                                December 23, 2004, 10:53:21 ; Search time 38 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-911-092-7
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US-08-485-101B-7
US-09-485-121A-7
US-09-252-991A-25518
US-09-252-991A-24427
US-09-252-991A-24427
US-09-252-991A-24427
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US-09-252-991A-2628
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US-09-315-794-42
US-09-252-991A-2998
US-09-252-991A-2998
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US-09-252-991A-18940
US-09-252-991A-23167
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                                                                                                                                                                                                                                                             478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                              Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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                                                                                                                                                        Title:
Perfect score;
Sequence:
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Maximum DB
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No.
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Sequence 7, Application US/08489666C

Patent No. 5522600

GENERAL INFORMATION:

APPLICANT: No. 592600eborn, M.H.M

APPLICANT: Koch, G.

TITLE OF INVENTION: Chicken Anemia Virus mutants and

TITLE OF INVENTION: vaccines and uses based on the viral proteins VP1, VP2 (TITLE OF INVENTION: VP3 or sequences of that virus coding therefor.)

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAE-VENTER LAW, P.C.

STREET: 260 SHERIDAN AVE., P.O. BOX 60039
                                                    Appli
Appli
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                                                                                                                                           Sequence 3, Appli
Sequence 3, Appli
Sequence 44, Appl
Sequence 17435, A
Sequence 28280, A
Sequence 27629, A
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Sequence
Sequence
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US-09-252-991A-23646
US-07-903-103-2
US-08-044-619A-2
US-08-283-911-2
US-08-390-546-3
US-08-390-646-3
US-08-390-515-3
US-08-390-515-3
US-08-390-515A-3
US-08-390-515A-3
US-08-801-718-3
US-09-170-159A-3
US-09-252-991A-17435
US-09-252-991A-27629
US-09-252-991A-27629
US-09-252-991A-27629
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  USA
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and

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61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
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Pred. No. 9.8e-66;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,001B
FILIGATION DATE: 07-UUNE-1995
      APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBY003.00US1
TELECHOMUNICATION INFORMATION:
TELEPHONE: (650) 328-4470
TELEFAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acids
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
FILING DATE: 30-NOVEMBER-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL94/00168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT/NL94/00168
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/030,335
PILING DATE: 8-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9301272
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.5%;
Best Local Similarity 99.2%;
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 L 121
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US-08-485-001B-7
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Sequence 7, Application US/08911092
Batenti NO. 5952002
GENERAL INFORMATION:
APPLICANT: NO. 5952002eborn, Matheus H.M.
APPLICANT: Noch; Guus
TITLE OF INVENTION: Chicken Anemia Virus Mutants And Vaccines
TITLE OF INVENTION: And Uses Based On The Viral Proteins VP1, VP2, And VP3 Or
TITLE OF INVENTION: Sequences Of That Virus Coding Therefor
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Rea-Venter Law Group, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                               61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                    1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
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                                                                                                                                                                                                                                              Length 121;
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MEDIUM TYPE: B. F10ppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
SUSTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/911,092
FILING DATE: 14-A06-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
FILING DATE: 30-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/NL94/00168
FILING DATE: 19-UULY-1994
PRIOR APPLICATION NUMBER: NL 9301272
FILING DATE: 0-UULY-1993
PRIOR APPLICATION NUMBER: US 08/030,335
FILING DATE: 0-UULY-1993
RIOR APPLICATION NUMBER: US 08/030,335
FILING DATE: B-MAR-1993
CLASSIFICATION NUMBER: PCT/NL91/00165
FILING DATE: 11-SEP-1991
                                                                                                                                                                                                                                                  99.5%; Score 629; DB 2; Lv 99.2%; Pred. No. 9.8e-66; iive 1; Mismatches 0;
             INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 121 amino acids TYPE: amino acid STRANDEDNESS: unknown TOPOLOGY: unknown MOLECULE TYPE: unknown MOLECULE TYPE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.O. Box 60039
(650)328-4477
                                                                                                                                                                                                                                                                      Best Local Similarity 99.2
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: California
COUNTRY: USA
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TELEFAX:
TELEX: N
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Gaps

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US-W82-101B-7

1 Sequence 7, Application US/08482161B

Patent No. 6162461

GENERAL INFORMATION

APPLICANT: No. 6164461eborn, Matheus H.M.

APPLICANTON: Sequences Of That Virus Coding Therefor

NUMBER OF ESQUENCES: 30

CORRESPONDENCE ADDRESS: 40

CONNTRY: USE California

COUNTRY: USE California

COMPUTER: EMP PC compatible

COMPUTER: EMP PC compatible

COMPUTER: EMP PC compatible

OPERATIOS YSTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US 08/482,161B

FILING DATE: 07-UUNE-1995

CLASSIFICATION NUMBER: US 08/454,121

PRIOR APPLICATION NUMBER: US 08/454,121

PRIOR APPLICATION NUMBER: US 08/454,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TADNSESTGFKOVPDLRIDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRIR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNALQEDIPPGPSTVFRPPISSRPIETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.5%; Score 629; DB 3; Length 121; Best Local Similarity 99.2%; Pred. No. 9.8e-66; Matches 120; Conservative 1; Mismatches 0; Indels
             PELLING DATE: 8-MAR-1993
PRIOR APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: PT/NL91/00165
PILING DATE: 1-SEP-1991
PRIOR APPLICATION NUMBER: PT/NL91/00165
PILING DATE: 11-SEP-1991
PRIOR APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rac-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV.003.00US
TELECOMMUNICATION INFORMATION:
TELEFPHONE: (650) 328-4400
TELEFPHONE: (650) 328-4400
TELEFPHONE: (650) 328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERICATICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 121 amino acida
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-454-121A-7
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Patent No. 6071520
GENERAL INFORMATION:
APPLICANT: No. 6071520eborn, Matheus H.M.
APPLICANT: Koch, Guus
TITLE OF INVENTION: Chicken Anemia Virus Mutants And Vaccines
TITLE OF INVENTION: Chicken Anemia Virus Coding Therefor
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,121A
PILING DATE: 07-JUNE-1995
PILOR APPLICATION 1435
PRIOR APPLICATION NUMBER: PCT/NL94/00168
PILING DATE: 19-JULY-1994
PRIOR APPLICATION NUMBER: RCT/NL94
PRIOR APPLICATION NUMBER: NL 9301272
FILING DATE: 20-JULY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 629; DB 2;
Pred. No. 9.8e-66;
                                                                                                                                                                                               NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REGISTRATION NUMBER: 1EBV.003.02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 926-6205
TELEFAX: (650) 424-8760
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Rae-Venter Law Group, P.C.
P.O. Box 60039
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL91/001-
FILING DATE: 11-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SEPTEMBER-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.5%;
20-JULY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. Box 60
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 120; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 L 121
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Gaps

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENITION: NUCLEELC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENITION: ALERGER AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PELLING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
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                 PRIOR APPLICATION: DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/489,666
FILING DATE: 07-01N-1995
FILING DATE: 07-01N-1995
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
FILING DATE: 30-000-1995
FILING DATE: 08-000-1995
FILING DATE: 08-00168
FILING DATE: 19-011-1994
FRICH APPLICATION NUMBER: PCT/NL 94/00168
FILING DATE: 19-01L-1994
FRICH APPLICATION DATA:
APPLICATION NUMBER: PCT/NL 91/00165
FILING DATE: 11-SEP-1991
FRICH APPLICATION DATA:
APPLICATION NUMBER: NL 9301272
FILING DATE: 12-SEP-1991
FRICH APPLICATION DATA:
APPLICATION NUMBER: NL 9301272
FILING DATE: 12-SEP-1990
ATTORNEY/AGENT INFORMATION:
FILING DATE: 13-SEP-1990
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acids
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Sequence 6, Application US/09057963A

Sequence 6, Application US/09057963A

Patent No. 6217870

GENERAL INFORMATION:
APPLICANT: No. 6217870eborn, M.H.M

APPLICANT: No. 6217870eborn, M.H.M

TITLE OF INVENTION: Chicken Anemia Virus mutants and
TITLE OF INVENTION: vaccines and uses based on the viral proteins VP1, VP2 and
TITLE OF INVENTION: vP3 or sequences of that virus coding therefor.
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Rae-Venter, Barbara
REGISTRATION VUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV.003.01US
TELECOMMUNICATION INPORMATION:
                 FILING DATE: 19-JULY-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 08-WARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9301272
FILING DATE: 20-JULY-1993
PRIOR APPLICATION NUMBER: PCT/NL 91/00165
FILING DATE: 11-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9002008
APPLICATION NUMBER: NL 9002008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: RAE-VENTER LAW GROUP, P.C. STREET: P.O. BOX 60039
CITY: PALO ALTO
APPLICATION NUMBER: PCT/NL 94/00168
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FILING DATE: 09-APR-1998
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 12-SEPTEMBER-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (650) 926-6205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 424-8760
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
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Best Local Similarity
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25561, Application US/09252991A
Patent No. 6551799.
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                     55 ---PILRSATADNSESTGFKNVPDLRIDQPKPPSKKRSCDPSEYRVSELKESLITITPSR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TADNSEST------GFKNVPDLRTDQPKPP-SKKRSCDPSEYRVSELKESLITTTPSR 111
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                                                                                                                                                                                                        9 PPGPSTVFRPPTS-SRPLETP------HCREIRIGIAGITITLSLCGCANARA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Indels 34; Gaps
                                                                                                                         Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 488;
                                                                                                                                                                   53; Indels
                                                                                                                                                                                                                                                                                                                                   432 GRRPGORSGSRRRPARPRRAPGPPRRTDQGOPRLHROPCRP----
                                                                                                                         13.7%; Score 86.5; DB 4; 27.9%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.4%; Score 85; DB 4;
Best Local Similarity 30.3%; Pred. No. 0.18;
Matches 37; Conservative 10; Mismatches
                                                                                                                                                                13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR PILING DATE: 1998-02-18
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-07-27
SEQ ID NO 30531
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                          Best Local Similarity 27.9% Matches 36; Conservative
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482 PRRRRRRMR 490
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                                                                             US-09-252-991A-25918
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US-09-252-991A-25561
SEQ ID NO 25918
                                                                                                                         Query Match
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUCIANGE FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERBNCE: 107196,136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR PAPLICATION NUMBER: US 60/094,190 PRIOR PAPLICATION NUMBER: US 60/094,190 NUMBER OF SEQ ID NOS: 33142 SEQ ID NOS: 33142
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 SRFMRKTARRKTPSTTANRPTPPS-----PTPTRASR------PRPRATRRKSRV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PTPSTPAIPTSSCRR-TVGIA----TAATSCSNPTKARTTRSASRVNISTDDSIPVSPT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---STVFRPPTSS----RPLETPHCREIRIGIAGITITLSLCGC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 TPPWPTLREKSNSSGSTSASSVRRSPRASSRTRRACSSPRC-----TLSASICRC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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25.0%; Pred. No. 0.2;
.ive 21; Mismatches 36; Indels 57
                                                                                                                                                                                                                                                                                                                        ch 13.2%; Score 83.5; DB 4; Length 133; 1 Similarity 27.5%; Pred. No. 0.048; 33; Conservative 12; Mismatches 36; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                             19 PTSSRP-LETPHCREIRIGIAGITITLSLCGCAN-ARAPTLRSATADN
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PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR PLING DATE: 1998-02-18 PRIOR PILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 25561 LENGTH: 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24427, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 27628, Application US/09252991A ; Patent No. 6551795
                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Pseudomonas aeruginosa US-09-252-991A-24427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.09
Matches 38; Conservative
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Best Local Similarity
Matches 33; Conserv
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US-09-252-991A-24427
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Sequence 26956, Application US/09252991A

Sequence 26956, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-07-27
                                                                                                                                                                                                                                   7 DTPPGPSTVFRPPTSSR-PLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 56334, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 DIPPGPSTVFRPPISSR-PLEIPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNS
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-----SRSPSRRTSTNLNT
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                                                                                                                                                                                                                                                                                                                                 66 ESTGFKNVPD----LRTDQPKP-PSKKRSCDPSEYRVSELKESLITTTPSRPRTAR 116
                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.8%; Score 81; DB 4; Length 160; 26.7%; Pred. No. 0.12; ive 15; Mismatches 38; Indels
                                                                                                                                                                                    38; Indels
                                                                                                                                Score 81; DB 4
Pred. No. 0.12;
                                                                                                                                                                                    15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 EKPQGKSP---SPTSSRSPSRSP----
                                                         ; ORGANISM: Drosophila melanogaster US-09-270-767-41118
                                                                                                                                                                                                                                                                               9 EKPQGKSP---SPTSSRSPSRSP
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1 Similarity 26.7%;
31; Conservative 1
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SEQ ID NO 26926
LENGTH: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Conservative
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                Query Match
Best Local Similarity
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Best Local Similarity
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          LENGIH: 160
                                 TYPE: PRT
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: NOTUBER OF ENDINORMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SOO ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                          45 SLCGCANARAPTLRSATADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 PTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLR-----SATADNSESTGFKNV 73
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: TO SO 1936-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1990-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4118
                                                                                                                                                                                                                                                                                                                                                                                                                                         17 SRCRCTPSTTST-NTSSASRTSST----APAPRASRPTPSS-----PNPHRRSSRSTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 PTSIR-----CRSISVACRARSIICPMCWPTTRRRPTRRTISCGSALGCIROSRRCRST
                                                                                                                                                                                                                                                                                                                                                              11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
12.9%; Score 81.5; DB 4; Length 135;
Best Local Similarity 27.8%; Pred. No. 0.083;
Matches 32; Conservative 12; Mismatches 42; Indels 29;
                                                                                                                                                                                                                                                                                                         Length 222;
                                                                                                                                                                                                                                                                                                                                                           28; Indels
                                                                                                                                                                                                                                                                                                         Score 82.5; DB 4;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 27628
LENGTH: 222
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; Sequence 41118
; Patent No. 6703491
; GENERAL INFORMATION:
                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29784
                                                                                                                                                                                                                                                                                                         Query Match 13.1%;
Best Local Similarity 33.3%;
Matches 24; Conservative
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LENGTH: 135
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632
1 MNALQEDTPPGPSTVFRPPT.......BSLITTTPSRPRTARRIRL 121
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1: \( \cgn2 \frac{6}\) ptodata/2\\ pubpaa/USO7 \trace{PUBCOMB.pep:*}

2: \( \cgn2 \frac{6}\) ptodata/2\\ pubpaa/USO7 \trace{PUBCOMB.pep:*}

2: \( \cgn2 \frac{6}\) ptodata/2\\ pubpaa/USO6 \trace{NEW PUB.pep:*}

4: \( \cgn2 \frac{6}\) ptodata/2\\ pubpaa/USO6 \trace{NEW PUB.pep:*}

5: \( \cgn2 \frac{6}\) ptodata/2\\ pubpaa/USO6 \trace{NEW PUB.pep:*}

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8: \( \cgn2 \frac{6}\) ptodata/2\\ pubpaa/USO9 \trace{NECOMB.pep:*}

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10: \( \cgn2 \frac{6}\) ptodata/2\\ pubpaa/USO9 \trace{NECOMB.pep:*}

11: \( \cgn2 \frac{6}\) ptodata/2\\ pubpaa/USO9 \trace{NECOMB.pep:*}

13: \( \cgn2 \frac{6}\) ptodata/2\\ pubpaa/USO9 \trace{NECOMB.pep:*}

13: \( \cgn2 \frace{6}\) ptodata/2\\ pubpaa/USO9 \trace{NECOMB.pep:*}

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16: \( \cgn2 \frace{6}\) ptodata/2\\ pubpaa/USIO \trace{NECOMB.pep:*}

17: \( \cgn2 \frace{6}\) ptodata/2\\ pubpaa/USIO \trace{NECOMB.pep:*}

18: \( \cgn2 \frace{6}\) ptodata/2\\ pubpaa/USIO \trace{NECOMB.pep:*}

18: \( \cgn2 \frace{6}\) ptodata/2\\ pubpaa/USIO \trace{NECOMB.pep:*}

18: \( \cgn2 \frace{6}\) ptodata/2\\ pubpaa/USIO \trace{NECOMB.pep:*}

19: \( \cgn2 \frace{6}\) ptodata/2\\ pubpaa/USIO \trace{NECOMB.pep:*}

19: \( \cgn2 \frace{6}\) ptodata/2\\ pubpaa/USIO \trace{NECOMB.pep:*}

19: \( \cgn2 \frace{6}\) ptodata/2\\ pubpaa/USIO \trace{NECOMB.pep:*}

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Appli	Appli	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	, Appl	Ann
		_	[7	7	10,	11,	12,	14,	15,	16	13	17,	18,	19,	ď
		Description	Sequence	Sequence 19,	a Charles										
			-1-	-2	-10	-11	-12	-14	-15	-16	-13	-17	-18	-19	a
COLUMNIC			-083-849B	US-10-083-849B-19	-738-423-										
-		Ω	US-10	110-10											
		DB	14	14	14	14	14	14	14	14	14	14	14	14	,
		Length	121	121	121	121	121	121	121	121	121	121	121	121	134
	* Query	Match	100.0	99.5	99.2	99.3	99.2	99.1	99.1	99.1	98.7	98.4	98.4	98.4	00
		Score	632	629	627	627	627	626	626	626	624	622	622	622	103
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Sequence 60, Appl	Sequence 1, Appli	Sequence 4, Appli			ø	Sequence 6, Appli	Sequence 8, Appli	Sequence 7, Appli	Seguence 9, Appli	Sequence 3, Appli	Sequence 4, Appli	Seguence 190571,	Sequence 163025,		Sequence 108424,						Sequence 165015,					Ŋ		-			Sequence 66407, A
	US-1	US-09-949-780-4	US-09-949-780-6	US-09-949-780-2	4 US-10-083-849B-5		4 US-10-083-849B-8		4 US-10-083-849B-9	us-	4 US-10-083-849B-4		ns-	6 US-10-437-963-120157	10-4		US-10-4					us-	US-10	6 US-10-767-701-57343	US-10-437-963-1	us-	US-10-43	US-10-7	US-10-437-963	US-10-425-115-222	5 US-10-425-114-66407
140 1	523 13	133 9	195 9	511 9	Н	Н	-	Н	٦	121 1	-	٦	٦	Н	٦	Н	335 1					ın	168 1				195 10	210 16	897 10	<u>~</u>	315 1
621 98.3	98.3	616 97.5	97.5	97.5	96.2	96.0	96.0	95.9	92.6	602 95.3	94.6	3 16.3	14.8	.2	13.5	4.	13.1	3 13.1	3 13.1	۲.	-	2 13.0	٥.	6	1.5 12.9	12.9 5	12.8	12.8	1 12.8	5 12.7	80.5 12.7
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	. 38	39	40	41	42	43	44	45

ALIGNMENTS

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US-10-083-849B-1

Sequence 1, Application US/10083849B

PUBLICANIENCE OF US2030199009A1

GENERAL INPOWATION

APPLICANT: No. US2030199009A1eborn, Mathieu

APPLICANT: No. US2030199009A1eborn, Mathieu

APPLICANT: Rohn, Jennifer Leigh

APPLICANT: Dominar, Peter

TUTLE OF INVENTION: Modifications of Apoptin

FILE REFERENCE: 2906-4936.1

FURNERT FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: US/10/083,849B

CURRENT FILING DATE: 2000-10-20

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Ratentin version 3.1

TYPE: PRT

TYPE: PRT

TYPE: PRT

TYPE: PRT

TYPE: PRT

TYPE: PRT

ORANISM: Chicken anemia virus

FEATURE:

LOCATION: (1). [121)

OTHER INFORMATION: Aboptin (a small protein derived from chicken anemia virus)

COTHER INFORMATION: Aboptin (a small protein derived from chicken anemia virus)

OTHER INFORMATION: Aboptin (a small protein derived from chicken anemia virus)

OTHER INFORMATION: Aboptin (a small protein derived from chicken anemia virus)

OTHER INFORMATION: Aboptin (a small protein derived from chicken anemia virus)

OTHER INFORMATION: Aboptin (a small protein derived from chicken anemia virus)

MATCHES 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DD

I MALQEDTPEORSTVERPPESREPLETPHCREIRIGIAGITITLELCGCANARAPTLRSA 60

INALQEDTPEORSTVERPPESREPHERPHRERHIGIAGITITLELCGCANARAPTLRSA 60
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61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRRIR 120
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LOCATION: (1)..(121)
OTHER INFORMATION: single point mutant T106A of Apoptin
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OTHER INFORMATION: single point mutant T107A of Apoptin
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99.2%; Score 627; DB 14;
Best Local Similarity 99.2%; Pred. No. 5.7e-55;
Matches 120; Conservative 0; Mismatches 1;
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Pred. No. 5.7e-55;
0; Mismatches 1;
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; Publication No. US20030199009A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030199009Aleborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
; APPLICANT: Mumberg, Dominik
; APPLICANT: Domner, Peter
; TILE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4966.1
; CURRENT APPLICATION NUMBER: US/10/083,849B
; CURRENT APPLICATION NUMBER: US 60/242,397
; PRIOR APPLICATION NUMBER: US 60/242,397
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 11
                                                                                 TYPE: PRT ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Chicken anemia virus
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 121
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Best Local Similarity 99.2%;
Matches 120; Conservative
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        61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
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OTHER INFORMATION: Apoptin protein encoded by pIRESneo alanine mutants
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                                                                                                                                                                                                                                                     Sequence 2, Application US/10083849B
Publication No. US20030199009A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. US20030199009Aleborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Muhberg, Dominik
APPLICANT: Muhberg, Dominik
APPLICANT: Muhberg, Dominik
APPLICANT: Domner, Peter
ITILE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996.1
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR APPLICATION NUMBER: US 60/242,397
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
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Publication No. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, 10minik
APPLICANT: Mumberg, 20061496.1
ITLE OF INVENTION: Modifications of Apoptin
FILE OF INVENTION: Modifications of Apoptin
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
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LENGTH: 121
TYPE: PRT
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1; Indels
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; OTHER INFORMATION: single point mutant T107E of Apoptin
US-10-083-849B-15
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99.1%; Score 626; DB 14;
Best Local Similarity 99.2%; Pred. No. 7.2e-55;
Matches 120; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/10083849B
FUDLICATION O. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: No. US20030199009Aleborn, Mathieu
APPLICANT: Nohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, Dominik
TILE REFERENCE: 2906-4996.1
FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT APPLICATION NUMBER: US 60/242,397
FRIOR APPLICATION NUMBER: US 60/242,397
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATCHIN VERSION 3.1
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; Publication No. US20030199009A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030199009Aleborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
; APPLICANT: Mumberg, Dominik
; APPLICANT: Donner, Peter
; TITLE OF INVENTION: Modifications of Apoptin
; FILE REFERENCE: 2906-4996.1
; CURRENT APPLICATION NUMBER: US/10/083,849B
; CURRENT PILING DATE: 2001-10-19
0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/242,397
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ORGANISM: Chicken anemia virus
Matches 120; Conservative
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US-10-083-849B-16
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Pred. No. 5.7e-55;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)..(121)
; OTHER INFORMATION: single point mutant T108A of Apoptin
US-10-083-849B-12
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; OTHER INFORMATION: single point mutant T106E of Apoptin US-10-083-849B-14
                                  Sequence 12, Application US/10083849B
Publication No. US20030199009A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. US20030199009Aleborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Muhberg, Dominik
APPLICANT: Domner, Peter
ITILE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996-1
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
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Publication No. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, Dominik
APPLICANT: Peter
ITLE OF INVENTION: Modifications of Apoptin
FILE REFRENCE: 2906-4996-1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
FRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
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Best Local Similarity 99.2%
Matches 120; Conservative
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Best Local Similarity
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LENGTH: 121
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LENGTH: 121
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61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)..(121)
; OTHER INFORMATION: double point mutation T106A107A of Apoptin US-10-083-849B-17
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; OTHER INFORMATION: double point mutant T107A108A of Apoptin
US-10-083-849B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 98.4%; Score 622; DB 14;
Best Local Similarity 98.3%; Pred. No. 1.8e-54;
Matches 119; Conservative 0; Mismatches 2;
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PUBLICATION NO. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
ITILE OF INVENTION: Modifications of Apoptin
FILE OF INVENTION: Modifications of Apoptin
FILE OF INVENTION: WOMER: US/10/083,849B
CURRENT APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 121
                                                               Sequence 17, Application US/10093849B; Publication No. US2003019900941; GRUERAL INFORMATION:
GREERAL INFORMATION:
APPLICANT: No. US20031099009Aleborn, Mathieu APPLICANT: Rohn, Jennifer Leigh APPLICANT: Donner, Peter TITLE REFERENCE: 2906-4996.1
TITLE REFERENCE: 2906-4996.1
CURRENT APPLICANTON NUMBER: US/10/083,849B; CURRENT FILING DATE: 2001-10-19; PRIOR APPLICATION NUMBER: US 60/242,397; PRIOR APPLICATION NUMBER: US 60/242,397; SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Chicken anemia virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MUTAGEN
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US-10-083-849B-18
                                                       US-10-083-849B-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.7%; Score 624; DB 14; Length 121; 99.2%; Pred. No. 1.1e-54; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                      NAME/KEY: MUTAGEN
LOCATION: (1)..(121)
COTENTION: (1)..(121)
OTHER INDEPENDATION: Single point mutant T108E of Apoptin US-10-083-8498-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)...(121)
CTHER INFORMATION: single point mutant P109A of Apoptin US-10-083-849B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/10083849B
; Bublication No. US20030199009A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030199009A1
; APPLICANT: Rohn, Jennier Leigh
; APPLICANT: Rohn, Jennier Leigh
; APPLICANT: Mumberg, Dominik
; APPLICANT: Mumberg, Dominik
; APPLICANT: Donner, Peter
; TITLE OF INVENTION: Modifications of Apoptin
; FILE FEFRENCE: 2906-4996.1
; CURRENT APPLICATION NUMBER: US/10/083,849B
; CURRENT APPLICATION NUMBER: US 60/242,397
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Chicken anemia virus
                                                                                                                                                         ORGANISM: Chicken anemia virus
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 116
LENGTH: 121
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Best Local Similarity 99.2'
Matches 120; Conservative
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APPLICANT: Clairmont, C.
APPLICANT: Lin, S.
APPLICANT: Lin, S.
APPLICANT: Belcourt, M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
FILE REPERENCE: 8002-0599
CURRENT APPLICATION NUMBER: US/10/738,423
CURRENT FILING DATE: 2003-12-16
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 1999-10-04
PRIOR PLILNG DATE: 1999-10-04
PRIOR PILING DATE: 1999-10-04
PRIOR PILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 61
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Best Local Similarity 98.3%; Pred. No. 2.7e-54;
Matches 119; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                              Score 621; DB 17;
Pred. No. 2.6e-54;
1; Mismatches 1;
  CURRENT FILLING DATE: 2003-12-16

PRIOR APPLICATION NUMBER: US/09/645,415

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: 60/157,581

PRIOR PELING DATE: 1999-10-04

PRIOR PLILING DATE: 1999-10-04

PRIOR PLILING DATE: 1999-10-04

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PASESEQ for Windows Version 3.0

SEQ ID NO 59
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; Sequence 60, Application US/10738423
; Publication No. US20040229338A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    98.3%;
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Best Local Similarity 98.3
Matches 119; Conservative
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                                                                                                      1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITILILSLCGCANARAPTLRSA 60
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Sequence 58, Application US/10738423

Publication No. US20040229338A1

GENERAL INFORMATION:
APPLICANT: King, I.
APPLICANT: Lin, S.
APPLICANT: Belcourt, M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS TARGETED DELIVERY OF EFFECTOR MOLECULES
FILE REFERENCE: 8002-059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.4%; Score 622; DB 14; Length 121; 98.3%; Pred. No. 1.8e-54; cive 0; Mismatches 2; Indels (
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LOCATION: (1)..(121)
CTHER INFORMATION: double point mutant T106A108A of Apoptin
US-10-083-849B-19
  98.3%; Pred. No. 1.8e-54;
live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: No. US20030199009Aleborn, Mathieu APPLICANT: Rohn, Jennifer Leigh APPLICANT: Rumberg, Dominik APPLICANT: Mumberg, Dominik APPLICANT: Dominer, Peter TITLE OF INVENTION: Modifications of Apoptin FILE REFRENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/10083849B
Publication No. US20030199009A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
Best Local Similarity 98.3
Matches 119; Conservative
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Best Local Similarity 98.3
Matches 119; Conservative
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Sequence 1, Application US/10113790
Sequence 1, Application US/10113790
Sequence 1, Application No. US20020176860A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. US20020176860A1eborn, Mathieu H.M.
APPLICANT: Zhang, Ying-Hui
APPLICANT: Zhang, Ying-Hui
APPLICANT: Zhang, Ying-Hui
APPLICANT: Trung OF 1005 No 1005
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98.3%; Score 621; DB 13; Length 523;
Best Local Similarity 98.3%; Pred. No. 1.3e-53;
Matches 119; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence FEATURE: FEATURE: 1 PEATURE: 1 OTHER HISPRATION: Apoptin-TK fusion protein US-10-113-790-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 23, 2004, 11:16:00 Job time: 146 secs
121 L 121
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

December 23, 2004, 10:52:36; Search time 39 Seconds (without alignments) 298.519 Million cell updates/sec

US-10-083-849B-1 632 1 MNALQEDTPPGPSTVFRPPT.......ESLITTTPSRPRTARRIRL 121 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	629	99.5	121		B39926	hypothetical prote
7	919	97.5	121	~	B48343	٦
٣	84	13.3	247	~	T32514	
4	83	13.1	377	~	A48018	
	81.5	12.9	982	~	T13653	hypothetical prote
9	80.5	12.7	748	~	D84595	pEARLI 4 protein [
7	80.5	12.7	3570	~	T45025	mucin MUC5B, trach
80	80	12.7	1388	α	A53317	collagen alpha 1(X
σ	79.5	12.6		~	S28394	probable serine/th
10	79.5	12.6		~	T15269	hypothetical prote
11	78.5	12.4		~	D70752	
12	78.5	12.4	475	~	D86209	
13	78.5	12.4	587	~	T29324	hypothetical prote
14	78	12.3	278	~	T46458	
15	77	12.2		~	S38148	hypothetical prote
16	76.5	12.1	182	N	T30760	hypothetical prote
17	76.5	12.1	417	~	S47539	homeotic protein H
18	76.5	12.1	587	~	T19893	hypothetical prote
19	76.5	12.1		~	T09219	basal transcriptio
20	75.5	11.9		~	S47091	cyclase-associated
21	75.5	11.9	669	7	C43674	US4 protein - huma
22	75	11.9	•	~	T17221	hypothetical prote
23	74.5	11.8	m	~	A41558	
24	74	11.7	4	٦	S24354	p53-binding protei
25	73.5		786	Н	A47547	
56	73	11.6		~	S62349	L71-3 protein - fr
27	73	•		~	S36488	E2 protein - human
28	73	11.6	631	~	A54659	DNA repair protein
29	72.5	11.5	416	~	S27198	homeotic protein H

mucin 2 precursor, hypothetical prote	hypothetical prote DNA (cytosine-5-)-	E2 protein - human hypothetical prote	nascent polypeptid	homeotic protein H glycoprotein G - B	hypothetical prote	hypothetical prote	nypornetical prote 35K proline-rich p	hypothetical prote	104K microneme-rho	KIAA0013 protein [
A43932 S40766	T22845 JE0378	W2WL47 T29776	T30826	S34164 S49525	T48107	T25592	134513 A56561	T36204	A44945	A59431
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3020	1250	506 1046	2187	411 593	975	1624	315	407	924	1023
11.5	11.4	11.3	11.3	11.2	11.2	11:2	11.2	11.2	11.2	11.2
72.5	27.	71.5	71.5	22	71	17	70.5	70.5	70.5	70.5
30 31	33	34 35	36	37 38	39	40	4 4 7	43	44	45

ALIGNMENTS

RESULT 1

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hypothetical protein 2 - chicken anemia virus
CiSpecies: chicken anemia virus, CAV
CiSpecies: chicken anemia virus, CAV
CiSpecies: chicken anemia virus, CAV
CiSpecies: 0.01-2004
CiSpecies: 0.01-2004
CiSpace: 0.01-2004
Cisp
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B39926
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ö Gape ö Score 629; DB 2; Length 121; Pred. No. 2.1e-52; 1; Mismatches 0; Indels Query Match 99.5 Best Local Similarity 99.2 Matches 120; Conservative

121 L 121 121 L 121 셤 ઠે

B48343

hypothetical 13K protein - chicken anemia virus (isolate Cux-1)
C;Species: chicken anemia virus, CAV
C;Species: 17-Feb-1994 #sequence_revision 16-Apr-1999 #text_change 09-Jul-2004
C;Accession: B48343
R;Meehan, B.M.; Todd, D.; Creelan, J.L.; Barle, J.A.; Hoey, E.M.; McNulty, M.S.
Arch. Virol. 124, 301-319, 1992
A;Title: Characterization of viral DNAs from cells infected with chicken anaemia agent:

A;Accession: B48343
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-121 cMEE>
A;Cross-references: UNIPROT:Q99152; GB:M81223; NID:g323254; PIDN:AAA42883.1; PID:g32325
A;Note: the authors translated the codon ACA for residue 41 as Gly
A;Note: sequence extracted from NCBI backbone (NCBIN:106168, NCBIP:106170)

97.5%; Score 616; DB 2; Length 121;

Query Match

#status predicted

4;

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A;Accession: 52916
A;Accession: 52916
A;Residues: 'S',71-79','N',81-86,'XX',89,'X',91,'P' <RE2>
A;Accession: S29114
A;Molecule type: protein
A;Residues: 143-145,'X',147,'XXX',151-152,'X',154-158,'X',160-161,'A',163-164,'XX',167-7
G;Genetics:
A;Gene: GDB:MUC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 PTPPATTPAPPSSSAPPETTAAPPTPSATTPAPLSSSAPPETTÄVPPTPSATTLÜPSSA- 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 PPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNSEST
                                                                                                                                                                                                                                                                                           A,Cross-references: GDB:138799; OMIM:158375
A;Map position: 4q13-4q21
C;Keywords: glycoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>F;19-377/Product: mucin 7, salivary #status predicted <MAT>F;97,128,135,146,312/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 GPKNVPDLRIDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 13.1%; Score 83; DB 2; Length 377; Local Similarity 29.2%; Pred. No. 2.3; Losservative 8; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 ---SAPPETTAAPPTPSATTPAPPSSPAPQETTAAPITTPNSSPTT
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Best Local Similarity 26.9%
Matches 32; Conservative
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NyAlternate names: mucin, MG2; mucin, MG2a-T1; mucin, MG2a-T2; mucin, MG2b-T2

C;Species: Home saplems (man)

C;Date: 16-Feb-1994 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A48018; S29116; S29114

C;Accession: A48018; S29115; S29116; S29114

J. Biol. Chem. 268, 20563-20569, 1993

A;Title: MOlecular cloning, sequence, and specificity of expression of the gene encoding

A;Reference number: A48018; MUID:93388636; PMID:7690757

A;Accession: A48018

A;Residues: 1-377 < BOS

A;Residues: 1-377 < BOS

A;Cossion: As BOSE

A;Cossion: Agource: submandibular gland

A;Note: sequence extracted from NCBI backbone (NCBIN:137719, NCBIP:137720)

R;Reddy, M.S.; BoDek, L.A.; Haraszthy, G.G.; Blesbrock, A.R.; Levine, M.J.

B;Ochem. 13. 287, 639-643, 1992

A;Title: Structural features of the low-molecular-mass human salivary mucin.

A;Reference number: S29114; MUID:93075006; PMID:1445223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: TIN>
A;Residues: 1-277 <TIN>
A;Cross-references: UNIPROT:O44145; EMBL:AF036692; PIDN:AAB88324.1; GSFDB:GN00022; CESP:A;Experimental source: strain Bristol N2; clone C44B12
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                                                                                                                                                      1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32514
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                                                       Gaps
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A;Map position: 4
A;Introns: 28/1; 164/1; 192/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C44B12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 247;
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiTin-Wollam, A. submitted to the EMBL Data Library, December 1997 A;Description: The sequence of C. elegans cosmid C44B12. A;Reference number: Z21183
. 3.5e-51;
2;
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13.3%; Score 84; DB 2;
Best Local Similarity 29.7%; Pred. No. 1.2;
Matches 35; Conservative 13; Mismatches 46
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Mismatches
                         Pred. No.
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                         98.3%;
                                                  119; Conservative
                         Similarity
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Matches 11
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pEARLI 4 protein [imported] - Arabidopsis thaliana (5:5pecies: Arabidopsis thaliana (mouse-ear crees) (5:5pecies: Arabidopsis thaliana (mouse-ear crees) (5:5pecies: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 (5:5decession: D84595 (5:5decession: D8595 (5:5decession:
57
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R;Ramer, S.W.; Davis, R.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 452-456, 1993
A;Title: A dominant truncation allele identifies a gene, STB20, that encodes a putative
A;Reference number: A47324; MUID:93133807; PMID:8421676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
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                                                                                  A.Status: preliminary
A.Astatus: preliminary
A.Residus: 1-748 - STO>
A.Cross-references: UNIPROT:Q9SKR5; GB:AE002093; NID:g4803947; PIDN:AAD29820.1; GSPDB:GN
A.Gene: At2g20960
A.Map position: 2
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C; Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text_change 09-Jul-2004
C; Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text_change 09-Jul-2004
C; Accession: A53317; A33146; S28778
R; Kivirikko, S.; Heinaemaeki, P.; Rehn, M.; Honkanen, N.; Myers, J.C.; Pihlajaniemi, T.
J. Biol. Chem. 269, 4773-4779, 1994
A; Title: Primary structure of the alphal chain of human type XV collagen and exon-intron A; Reference number: A53317; MulD:94148920; PMID:8106446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Homo sapiens (man)
Cispecies: T4502
Ricession: T4502
A; Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat A; Reference number: Z22899; MUID:97166151; PMID:9013550
A; Accession: T4502
A; Rittle: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat A; Reference number: Z2899; MUID:97166151; PMID:9013550
A; Ratus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-3570 obs3>
A; Cross-references: EMBL:Z72496; NID:91834502; PIDN:CAA96577.1; PID:91834503
A;Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80.5; DE
Pred. No. 8.4;
9; Mismatches
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26.4%;
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28.8%;
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Best Local Similarity 26.4*
Matches 29; Conservative
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Best Local Similarity
Matches 36; Conserv
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A; Molecule type: mRNA
A; Residues: 1-1388 «KIV»
A; Residues: 1-1388 «KIV»
A; Cross-references: UNIPROT: P39059; GB:L25280
A; Cross-references: UNIPROT: P39059; GB:L25280
A; Note: nucleotide sequence and conceptual translation not complete
B; Muragaki, Y.; Abe, N.; Ninomiya, Y.; Olsen, B.R.; Ooshima, A.
J. Biol. Chem. 269, 4042-4046, 1994
A; Title: The human alpha1(XV) collagen chain contains a large amino-terminal non-triple
A; Reference number: A53146; MUD:94140817; PMID:8307960
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA

A; Residues: 1-9, 'S', 11-48, 'V', 50-94, 'A', 96-149, 'A', 151-203, 'V', 205-408, 'A', 410-569 < MUR

A; Residues: 1-9, 'S', 11-48, 'V', 50-94, 'A', 96-149, 'A', 151-203, 'V', 205-408, 'A', 410-569 < MUR

A; Cross-references: GB:D21230; NID:9415605; PIDN: BAA04762.1; PID:d1005294; PID:9460703

R; Myers, J.C.; Kivirikko, S.; Gordon, M.K.; Dion, A.S.; Pihlajaniemi, T.

R; Myers, J.C.; Kivirikko, S.; Gordon, M.K.; Dion, A.S.; Pihlajaniemi, T.

A; Title: Identification of a previously unknown human collagen chain, alphal(XV), charach, A; Reference number: $28778; MUID:93066196; PMID:1279671
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BMBO.J. 11, 4815-4824, 1992 A.; Thomas D.Y.; Whiteway, M. A.; Title: The protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the yeast pheromone reparation of the protein kinase homologue Ste20p is required to link the year pheromone reparation of the protein kinase homologue Ste20p is required to link the year pheromone reparation of the protein kinase homologue Ste20p is required to link the year pheromone reparation of the protein kinase homologue Ste20p is required to link the year pheromone reparation of the protein kinase homologue ste20p is required to link the year pheromon
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A;Residues: 1-939 <LEB>
A;Cross-references: UNIPROT:Q03497; EMBL:M94719; NID:g172746; PIDN:AAA35111.1; PID:g172
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A,Residues: 1-939 <PAV>
A,Cross-references: EMBL:U11581; NID:9508676; PIDN:AAB69747.1; PID:9508679; MIPS:YHL007.
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F;1-22/Domain: signal sequence #status predicted <SIG>
F;1-23/Domain: signal sequence #status predicted <MAT>
F;23-1388/Product: collagen alpha 1(XV) chain #status predicted <MAT>
F;216-1388/Region: multiplexin collagen carboxyl-terminal homologous
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Submitted to the EMBL Data Library, June 1994
A;Description: The sequence of S. cerevisiae cosmid L5018.
A;Reference number: 846798
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A; Residues: 544-640,'P',642-811,'P',813-1252 <MYE>
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Pred. No. 18;
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Best Local Similarity 25.5%;
Matches 35; Conservative 1
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A,Gene: GDB:COL15A1
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Cispecies: Mycobacterium tuberculosis
Cispecies: Mycobacterium tuberculosis
Cipate: 17-ul-1998 #eequence_revision 17-Jul-1998 #text_change 09-Jul-2004
Cipate: 17-ul-1998 #eequence_revision 17-Jul-1998 #text_change 09-Jul-2004
Cipate: 17-ul-1998 #eequence_revision 17-Jul-1998 #text_change 09-Jul-2004
Cipate: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamilin, N.; Holroyd, S. Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70752
A;Accession: D70752
A;Residues: 1-202 <COL>
A;Residues: 1-202 <COL>
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C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 PGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNSESTG
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                                                                                                                                                                               probable lprE protein - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 78.5; DB 2;
; Pred. No. 3.1;
16; Mismatches 39;
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Pred. No. 8;
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23.3%;
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23.0%;
          118
                                                       652 KİSTVVPMITRRR 664
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Best Local Similarity 23.0%
Matches 28; Conservative
          RTA-----RRR
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Best Local Similarity
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A;Map position: 1
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D70752
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A; Molecule type: DNA
A; Residues: 1-18, 'S', 20-133, 'M', 135-270, 'S', 272-939 «RAM»
A; Cross-references: EMBL:L04655; NID:g172585; PIDN:AA35038.1; PID:g172586
A; Note: sequence extracted from NCBI backbone (NCBIN:122769, NCBIP:122774)
R; Wu, C.; Whiteway, M.; Thomas, D.Y.; Leberer, E.
Biol. Chem. 270, 15984-15995, 1995
A; Title: Molecular characterization of Ste20p, a potential mitogen-activated protein or
A; Reference number: A57493; MUID:95332294; PMID:7608157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: EMBL:AF003386; NID:g2088833; PID:g2088836; PIDN:AAB54252.1; GSPDB:GN
A,Experimental source: strain Bristol N2; clone F59512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542 PASPKAISHPSTPAKSPQKTPQKKKEITPVEVKIEEIKEEEDVTPSQSPPATQTPRSRGR 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Caenorhabditis elegans
Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
Accession: T15269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 QEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADN
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A;Introns: 122/2; 193/2; 254/3; 306/3; 459/2; 819/3; 859/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
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A;Molecule type: DNA
A;Residues: 1-1082 <JOH>
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12.6%; Score 79.5; DB
Best Local Similarity 30.1%; Pred. No. 13;
Matches 37; Conservative 11; Mismatches
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Best Local Similarity 27.1%;
Matches 36; Conservative
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A; Residues: 757-784 < WUA>
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A;Map position: 2
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A;Molecule type: DNA
X;Residues: 1-348 e.ROH>
A;Cross-references: UNIPROT:P36152; BMBL:228296; NID:g486542; PID:g486543; GSPDB:GN0001
A;Experimental source: strain S288C
|||: :: : | | | | | | :: | | | | :: | | | | :: | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein YKR071c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
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submitted to the Protein Sequence Database, March 1994
A;Reference number: S37897
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                                                                                                   60 ATADNSESTGFKNVPDLRTDQPKPPSKK-----
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Pred. No.
                                                                                                                                                                                                                                           96 RVSELKESLITTTPSRPRTARR 118
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A;Gene: SGD:DRE2; MIPS:YKR071c
A;Cross-references: SGD:S0001779
A;Map position: 11R
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Best Local Similarity 33.3
Matches 18; Conservative
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A;Experimental source: strain Bristol N2; clone M01E11
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----PTMQSTASRISTLTA 105
                                                                   -----VFRPPTSSRPLETPHCREIRIGIAGITI 42
                                                                                                                                                                                                       -----PSKKRS 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pothetical protein M01E11.6 - Caenorhabditis elegans
Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein DKFZp434M102.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
   Gaps
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R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23028
A;Accession: T46458
A;Status: preliminary
   65;
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38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 ASTFRQLRTGRPPPPSTQRSTATSSLKPSVTRARPVAQKPILP 148
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                                                                                                                                                                                                    43 TLSLCGCANARAPTLRSATADNSESTGFKNVPDLRTDQPKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Pauley, A.; Gattung, S.
submitted to the BMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid MOIEII.
A;Reference number: Z20605
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A;Experimental source: adult testis; clone DKFZp434M102
C;Genetics: DKFZp434M102.1
A;Note: DKFZp434M102.1
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-587 <PAU>
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23.8%; Pred. No. 5;
tive 14; Mismatches
Mismatches
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Best Local Similarity 23.3%; Pred. No. 10;
Matches 24; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                           90 CDPSEY--RVSELKESLITTTPSRPRTARR 117
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C;Superfamily: kinesin motor domain homology
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12;
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Best Local Similarity 23.8*
Matches 34; Conservative
Conservative
                                                                2 NALQEDTPPGPST--
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35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                            "Pathogenicity, sequence and phylogenetic analysis of Malaysian Chicken anaemia virus obtained after low and high passages in MSB-1 cells.";
                                                                                                                                                                                                                                                                                                                                                                              PubMed=14648297;
Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
Md-Zain B.M., Kono Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 632; DB 2; Length 121;
100.0%; Pred. No. 7e-52;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhong L.K., Cheng H.Q., Yun L.L.;
Zhong L.K., Cheng H.Q., Yun L.L.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR190102; AAM736511;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR06685; CAV VP3.
ERMI; PP04711; CAV VP3.
ERMI; PP04711; CAV VP3.
ERMI; PR04711; CAV VP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kono Y.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                 Viruses, ssDNA viruses, Circoviridae, Gyrovirus
                                                                                                                                                                                                                                        121 AA
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Q91N90
Q91N93
Q91N93
Q91NA2
Q91NA8
Q91NB4
Q91NB7
Q91NC0
Q91NC0
Q91NC0
Q91NC7
AAH68157
                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 05-JUL-2004 (TrEMBLrel. 27,
                        00000000
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Matches 121; Conservative
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  Chicken anemia virus.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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  VP3 (Apoptin).
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P54095 chicken ane
Q6r533 chicken ane
Aar97919 chicken a
Q6gvg8 chicken ane
                                                                                       (without alignments)
358.868 Million cell updates/sec
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                                                                                                                        US-10-083-849B-1
632
1 MNALQEDTPPGPSTVFRPPT......BSLITTTPSRPRTARRIRL 121
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                                                                             December 23, 2004, 10:37:16 ; Search time 194 Seconds
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                       1825181 segs, 575374646 residues
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Maximum Match 100%
Listing first 45 summaries
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VP3 CAV82
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Q6R533
AAR97919
Q6GVG8
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VP3 CAVC1
Q9DWX2
041448
VP3 CAVCI
Q9DH80
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Q91N81
Q8JNK4
Q75ZF9
Q9WB33
Q9DWW8
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Q9DWW6
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Q91ZU6
Q9DWW9
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Match Length DB
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596.5
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Result è ö

RESULT 2

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61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
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                                                                                                                                                                                                                                                        Scott A.N.J., McNulty M.S., Todd D.,
"Characterisation of a chicken anaemia virus variant population that
resists neutralisation with a group-specific monoclonal antibody.";
Arch. Virol. 146:713-728(2001).

EMBL, AJ297682; CAC14788.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0015051; P:induction of apoptosis by virus; IEA.
PINTERPO; IPRO66858 CAV VP3.
Pfam: PF04771; CAV VP3.
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SEQUENCE FROM N.A.
MEDLINE=98001356; PubMed=9343191;
Mebhan B.M., Todd D., Creelan J.L., Connor T.J., McNulty M.S.;
"Investigation of the attenuation exhibited by a molecularly cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of viral DNAs from cells infected with chicken ansemia agent: sequence analysis of the cloned replicative form and transfection capabilities of cloned genome fragments."; Arch. Virol. 124:301-319(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of an attenuated chicken anaemia virus isolate following repeated cell culture passage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
Todd D., Connor T.J., Calvert V., Creelan J.L., Meehan B.M.,
McNulty M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-92296898; PubMed=1605740;
Mechan B.M., Todd D., Creelan J.L., Earle J.A.P., Hoey B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 629; DB 2; Length LL. Pred. No. 1.3e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF04771; CAV VP3; I. SEQUENCE 121 AA; 13284 MW; 82ABB3865CCBACE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
0rf3; 13 kDa protein (VP3).
                                                          Last sequence update)
Last annotation update)
                                                                                                                                          Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
NCBI_TaxID=12618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
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1; Mismatches
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\u00e4vian Pathol. 24:171-187(1995).
                                         Created)
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21296594; PubMed=11402858;
                                                          (TrEMBLrel. 16, (TrEMBLrel. 24,
                                     (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.5
Matches 120; Conservative
PRELIMINARY;
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                                                        01-MAR-2001
01-JUN-2003
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                                                                                                                         Name=VP3;
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                  Q9DWX2;
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                                                                                                                                                                                                                                                      SECUENCE FROM N.A.

MEDLINE-91237831; PubMed=1851873;

MEDLINE-91237831; PubMed=1851873;

Moteborn M.H.M., de Boer G.F., van Roozelaar D.J., Karreman C.,

Kranenburg O., Vos J.G., Jeurissen S.H.M., Hoeben R.C., Zantema A.,

Koch G., van Ormondt H., van der Eb A.J.;

"Characterization of cloned chicken anemia virus DNA that contains all
elements for the infectious replication cycle.";

J. Virol. 65:3131-3139(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I. FUNCTION: May act as transcriptional regulator. Induces apoptosis in infected cells. Element of infectious replication cycle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of viral DNAs from cells infected with chicken anamina apent: sequence analysis of the cloned replicative form and transfection capabilities of cloned genome fragments."; Arch. Virol. 124:301-319(1992).
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Meehan B.M., Todd D., Creelan J.L., Earle J.A.P., Hoey E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.5%; Score 629; DB 1; Length 121; 99.2%; Pred. No. 1.3e-51; ive 1; Mismatches 0; Indels
                                                                                                                                          70 70 F -> S (in Ref. 2).
116 116 K -> R (in Ref. 2).
118 118 R -> C (in Ref. 2).
121 AA, 13270 WW, D2AAB3869BC12A3E CRC64;
                                                                                            (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
                                                          121 AA.
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Pfam; PF04771; CAV VP3; 1.
Apoptosis; Nuclear protein.
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1eg 120; Conservative
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PIR; B48343; B48343.
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Chicken anemia virus.
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Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
NCBI_TaxID=12618;
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(TrEMBLrel. 16, I
(TrEMBLrel. 24, I
99.28;
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01-MAR-2001 (TrEMBLrel. 16,
05-JUL-2004 (TrEMBLrel. 27,
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chicken anemia virus isolate by utilizing a chimeric virus approach.";
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-!- FUNCTION: May act as transcriptional regulator. Induces apoptosis in infected cells. Element of infectious replication cycle.
-!- SUBCELLULAR LOCATION: Nuclear; nucleus of infected cells.
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                                                                                                                                               Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases EMBL; U66304; AACS8477.1; -
EMBL; AU536295; Chos (259.1; -
GO; GO:0042025; Chost cell nucleus; IEA.
GO; GO:019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR006858; CAV vP3.
Efam; PF0471; CAV vP3. 1.
SEQUENCE 121 AA; 13312 MW; E4AAB75960F2C5C5 CRC64;
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Viruses, ssbNA viruses, Circoviridae, Gyrovirus.
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Pfam; PF04771; CAV VP3; T.
Apoptosis; Nuclear protein.
                             Virol. 71:8362-8367(1997)
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                                                                                                SEQUENCE FROM N.A. Chowding A.R., Aini I., Hair-Bejo M., Jamaluddin A.A., Chowdinry S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A., Kono Y., Darus A., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quantitation of chicken anemia virus by competitive polymerase chain
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    "Pathogenicity, sequence and phylogenetic analysis of Malaysian
Chicken anaemia virus obtained after low and high passages in MSB-1
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Jadhao S.J., Pattnaik B., Toshniwal R.M., Dash B.B., Pradhan H.K.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 4e-51;
0; Mismatches 1; Indels
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Yamaguchi S., Kaji N., Munangandu H.M., Kojima C., Mase M.,
Tsukamoto K.;
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Spackman E., Rosenberger J.K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL; AF390038; AAL99896.1; --
EMBL; AF475908; AAL79914.1; --
EMBL; AF520788; AAM75347.1; --
EMBL; AF520788; AAM75347.1; --
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IFR06658; AVV VP3.
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SEQUENCE 121 AA; 13245 MW; D2AAB39C2BD61A3E CRC64;
                                                              Arch. Virol. 148:2437-2448(2003)
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EMBL, AF311900; AAK70849.2; -.
EMBL, AB046587; BAB19539.1; -.
EMBL, AB046589; BAB19642.1; -.
EMBL, AB046590; BAB19642.1; -.
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Best Local Similarity 99.2%;
Matches 120; Conservative
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EMBL; AF199501; AAF08299.1
EMBL; AF285882; AAK83007.1
EMBL; AF313470; AAG34178.1,
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                                                    Scott A.N.J., McMulty M.S., Todd D.;
"Characterisation of a chicken anaemia virus variant population that
resists neutralisation with a group-specific monoclonal antibody.";
Arch. Virol. 146,713-728 (2001).

EMBL; AJ297681; CAC14755.1; -.

GO; GO:0042025; Chost cell nucleus; IEA.
GO:0019051; Pinduction of apoptosis by virus; IEA.
InterPro; IPR006858; CAV VP3.
Pfam; PF04771; CAV VP3; I.
SEQUENCE 121 AA; 13329 MW; A471DFF69BD61A3F CRC64;
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MEDLINE=21195622; PubMed=11297698;
Yamaguchi S., Imada T., Kaji N., Mase M., Tsukamoto K., Tanimura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yuasa N.;
"Idėntification of a genetic determinant of pathogenicity in chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=14648297;
Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
Md-Zain B.M., Kono Y.;
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MEDLINE=21310375; PubMed=11417817;
Van (Santen V.L., Li L., Hoerr F.J., Lauerman L.H.;
"Genetic characterization of chicken anemia virus from commercial broiler chickens in Alabama.";
Avian Dis. 45:373-388(2001).
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Viruses, ssDNA viruses, Circoviridae, Gyrovirus.
NCBI_TaxID=12618;
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                                    MEDLINE=21296594; PubMed=11402858;
Scott A.N.J., McNulty M.S., Todd D.;
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J. Gen. Virol. 82:1233-1238(2001)
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
05-JUL-2004 (TrEMBLrel. 27,
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Submitted (OCT-1999)
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SEQUENCE FROM N.A.
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Islam R.M., Johne R., Raue R., Todd D., Mueller H.;
Submitred (UUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB027470; BAAR1983.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR06885; CAV VP3.
SEQUENCE 121 AA; 13272 MW; 72B7AE9C2BD60BBB CRC64;
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Okamura H., Sakaguchi M., Tokunaga E.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
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98.3%; Pred. No. 7.6e-51;
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Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
98.3%; Pred. No. 7.6e-51;
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                Matches 119; Conservative
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Matches 119; Conservative
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Best Local Similarity
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Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
PubMed=14648297;
Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
Md-Zain B.M., Kono Y.;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY040632; AAK829471;
GO; GO:00420125; C:host cell nucleus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR006858; CAV VP3.
Pfam; PF04771; CAV VP3;
SEQUENCE 121 AA; 13338 MW; CD34CA7E9BD61A3E CRC64;
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Imai K., Yamaguchi S.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB119448; BAD12197.1; -.
Interpro; IPR006858; CAV VP3.
Pfam; PF04771; CAV VP3; I.
SEQUENCE 121 AA; 13272 MW; DA0822253B28FADO CRC64;
                                                                                             01-00T-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Chicken anemia virus.
Chickes; ssDNA viruses; Circoviridae; Gyrovirus.
NCBI_TaxID=12618;
                                                                                                                                                                     Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
NCBI_TaxID=12618;
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99.2%; Pred. No. 4.9e-51;
iive 0; Mismatches 1.
                                                                    121 AA
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Arch. Virol. 148:2437-2448(2003).
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05-JUL-2004 (TrEMBLrel. 27,
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Best Local Similarity 99.23
Matches 120; Conservative
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SEQUENCE

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TADNSESTGFKAVVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRCIR 120
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MEDLINE=95297149; PubMed=7778281;

MEDLINE=95297149; Nukamura T., Ishihama A., Otaki Y.;

Kato A., Fujino M., Nakamura T., Ishihama A., Otaki Y.;

"Gene organization of chicken anemia virus.";

Virology 209:480-488(1995).

-i- FUNCTION: May act as transcriptional regulator. Induces apoptosis

-i- FUNCTION: May act as infections regulator. organization cycle.

-in infected cells. Element of infection cycle.
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                                                                                                                                               MEDLINE=21310375; PubMed=11417817; van Santen V.L., Li L., Hoerr R.J., Lauerman L.H.; van Santen V.L., Li L., Hoerr R.J., Lauerman L.H.; Genetic characterization of chicken anemia virus from commercial broiler chickens in Alabama."; Avian Dis. 45:373-388 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                               98.1%; Score 620; DB 2; Length 12
98.3%; Pred. No. 9.5e-51;
ive 0; Mismatches 2; Indels
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Chicken anemia virus (Japanese isolate 82-2) (CAV)
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
                                                                   Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
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01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                           FROM N.A.
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                                                                       Scott A.N.J., McNulty M.S., Todd D.;
"Characterisation of a chicken anaemia virus variant population that
"Characterisation of a chicken anaemia virus variant population that
aresists neutralisation with a group-specific monoclonal antibody.";
Arch. virol. 146:713-728(2001).
EMBL, AJ297666; CAC14770.1;
GO: GO: 0019051; P: October Cell nucleus; IEA.
GO: GO: 0019051; P: Induction of apoptosis by virus; IEA.
InterPro; PREOMOSES, CAV VP3.
Pfam; PPC4771; CAV VP3.
ERGUENCE 121 AA; 13240 MW; D7ABB05D37A61A3E CRC64;
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"Antigenic variation among Chicken anemia virus strains.";
"Autigenic variation among Chicken anemia virus strains.";
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB119448; BAJ12197.1; -.
SEQUENCE 121 AA; 13272 PW; DA0822253B28FADO CRC64;
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Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
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Query Match

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DR Pfam; PF04771; CAV_VP3; 1.

KW Apoptosis; Nuclear protein.

SQ SEQUENCE 121 AA; 13233 MW; C770839C2BD61A3E CRC64;

Query Match

Query Match

97.9%; Score 619; DB 1; Length 121;

Best Local Similarity 98.3%; Pred. No. 1.2e-50;

Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps

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Mis Pogo Blonk (USDIO)